Figure 1A
Neutrokine-α

```
  1  AAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGCACGCAGGAC   60

 61  ATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCC  120

121  CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGAGCAGTCACGCC  180
  1                                  M  D  D  S  T  E  R  E  Q  S  R  L    12

181  TTACTTCTTGCCTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGTTTCCATCCTCC  240
 13   T  S  C  L  K  K  R  E  E  M  K  L  K  E  C  V  S  I  L  P    32
                                                            CD-I

241  CACGGAAGGAAAGCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCT  300
 33   R  K  E  S  P  S  V  R  S  S  K  D  G  K  L  L  A  A  T  L    52
                CD-I

301  TGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCC  360
 53   L  L  A  L  L  S  C  C  L  T  V  V  S  F  Y  Q  V  A  A  L    72

361  TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGC  420
 73   Q  G  D  L  A  S  L  R  A  E  L  Q  G  H  H  A  E  K  L  P    92
              CD-II

421  CAGCAGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGAC  480
 93   A  G  A  G  A  P  K  A  G  L  E  E  A  P  A  V  T  A  G  L   112
              CD-III
                                          #
481  TGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA  540
113   K  I  F  E  P  P  A  P  G  E  G  N  S  S  Q  N  S  R  N  K   132

541  AGCGTGCCGTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAG  600
133   R  A  V  Q  G  P  E  E  T  V  T  Q  D  C  L  Q  L  I  A  D   152
                                                        CD-IV

601  ACAGTGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCT  660
153   S  E  T  P  T  I  Q  K  G  S  Y  T  F  V  P  W  L  L  S  F   172
                                                     CD-V

661  TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTT  720
173   K  R  G  S  A  L  E  E  K  E  N  K  I  L  V  K  E  T  G  Y   192
          CD-V                                   CD-VI

721  ACTTTTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAA  780
193   F  F  I  Y  G  Q  V  L  Y  T  D  K  T  Y  A  M  G  H  L  I   212
                   CD-VI                                  CD-VII

781  TTCAGAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGAT  840
213   Q  R  K  K  V  H  V  F  G  D  E  L  S  L  V  T  L  F  R  C   232
          CD-VII                                      CD-VIII
                                      #
841  GTATTCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAA  900
233   I  Q  N  M  P  E  T  L  P  N  N  S  C  Y  S  A  G  I  A  K   252
       CD-VIII                              CD-IX
```

Figure 1B
Neutrokine-α

```
901  AACTGGAAGAAGGAGATGAACTCCAACTTGCAATACCAAGAGAAAAATGCACAAATATCAC   960
253    L  E  E  G  D  E  L  Q  L  A  I  P  R  E  N  A  Q  I  S  L   272
                                CD-X

961  TGGATGGAGATGTCACATTTTTTGGTGCATTGAAACTGCTGTGACCTACTTACACCATGT   1020
273    D  G  D  V  T  F  F  G  A  L  K  L  L                       285
                             CD-XI

1021 CTGTAGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA   1080

1081 CCAAAAAAAAAAAAAAAAAA  1100
```

FIGURE 2A

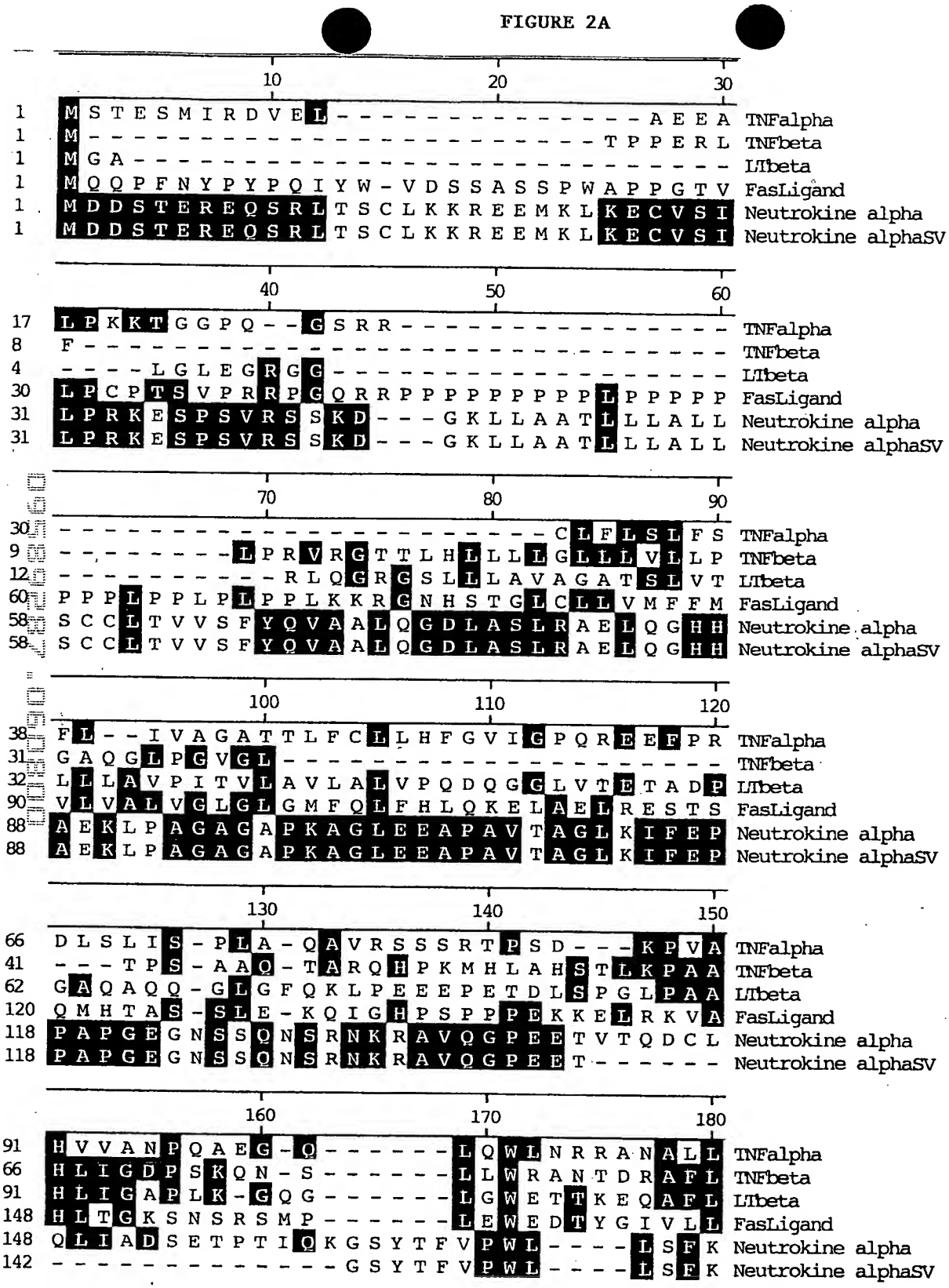

10 20 30
1 MSTESMIRDVEL----------AEEA TNFalpha
1 M----------TPPERL TNFbeta
1 MGA----------LTbeta
1 MQQPFNYPYPQIYW-VDSSASSPWAPPGTV FasLigand
1 MDDSTEREQSRLTSCLKKREEMKLKECVSI Neutrokine alpha
1 MDDSTEREQSRLTSCLKKREEMKLKECVSI Neutrokine alphaSV
40 50 60
17 LPKKTGGPQ--GSRR---------- TNFalpha
8 F---------- TNFbeta
4 ----LGLEGRGG---------- LTbeta
30 LPCPTSVPRRRPGQRRPPPPPPPPPLPPPPP FasLigand
31 LPRKESPSVRSSKD---GKLLAATLLLALL Neutrokine alpha
31 LPRKESPSVRSSKD---GKLLAATLLLALL Neutrokine alphaSV
70 80 90
30 ----------CLFLSLFS TNFalpha
9 ---------LPRVRGTTLHLLLLGLLLVLLP TNFbeta
12 ----------RLQGRGSLLLAVAGATSLVT LTbeta
60 PPPLPPLPLPPLKKRGNHSTGLCLLVMFFM FasLigand
58 SCCLTVVSFYQVAALQGDLASLRAELQGHH Neutrokine alpha
58 SCCLTVVSFYQVAALQGDLASLRAELQGHH Neutrokine alphaSV
100 110 120
38 FL--IVAGATTLFCLLHFGVIGPQREEFPR TNFalpha
31 GAQGLPGVGL---------- TNFbeta
32 LLLAVPITVLAVLALVPQDQGGLVTETADP LTbeta
90 VLVALVGLGLGMFQLFHLQKELAELRESTS FasLigand
88 AEKLPAGAGAPKAGLEEAPAVTAGLKIFEP Neutrokine alpha
88 AEKLPAGAGAPKAGLEEAPAVTAGLKIFEP Neutrokine alphaSV
130 140 150
66 DLSLIS-PLA-QAVRSSSRTPSD---KPVA TNFalpha
41 ---TPS-AAQ-TARQHPKMHLAHSTLKPAA TNFbeta
62 GAQAQQ-GLGFQKLPEEEPETDLSPGLPAA LTbeta
120 QMHTAS-SLE-KQIGHPSPPPEKKELRKVA FasLigand
118 PAPGEGNSSQNSRNKRAVQGPEETVTQDCL Neutrokine alpha
118 PAPGEGNSSQNSRNKRAVQGPEET------- Neutrokine alphaSV
160 170 180
91 HVVANPQAEG-Q------LQWLNRRANALL TNFalpha
66 HLIGDPSKQN-S------LLWRANTDRAFL TNFbeta
91 HLIGAPLK-GQG------LGWETTKEQAFL LTbeta
148 HLTGKSNSRSMP------LEWEDTYGIVLL FasLigand
148 QLIADSETPTIQKGSYTFVPWL----LSFK Neutrokine alpha
142 ----------GSYTFVPWL----LSFK Neutrokine alphaSV

FIGURE 2B

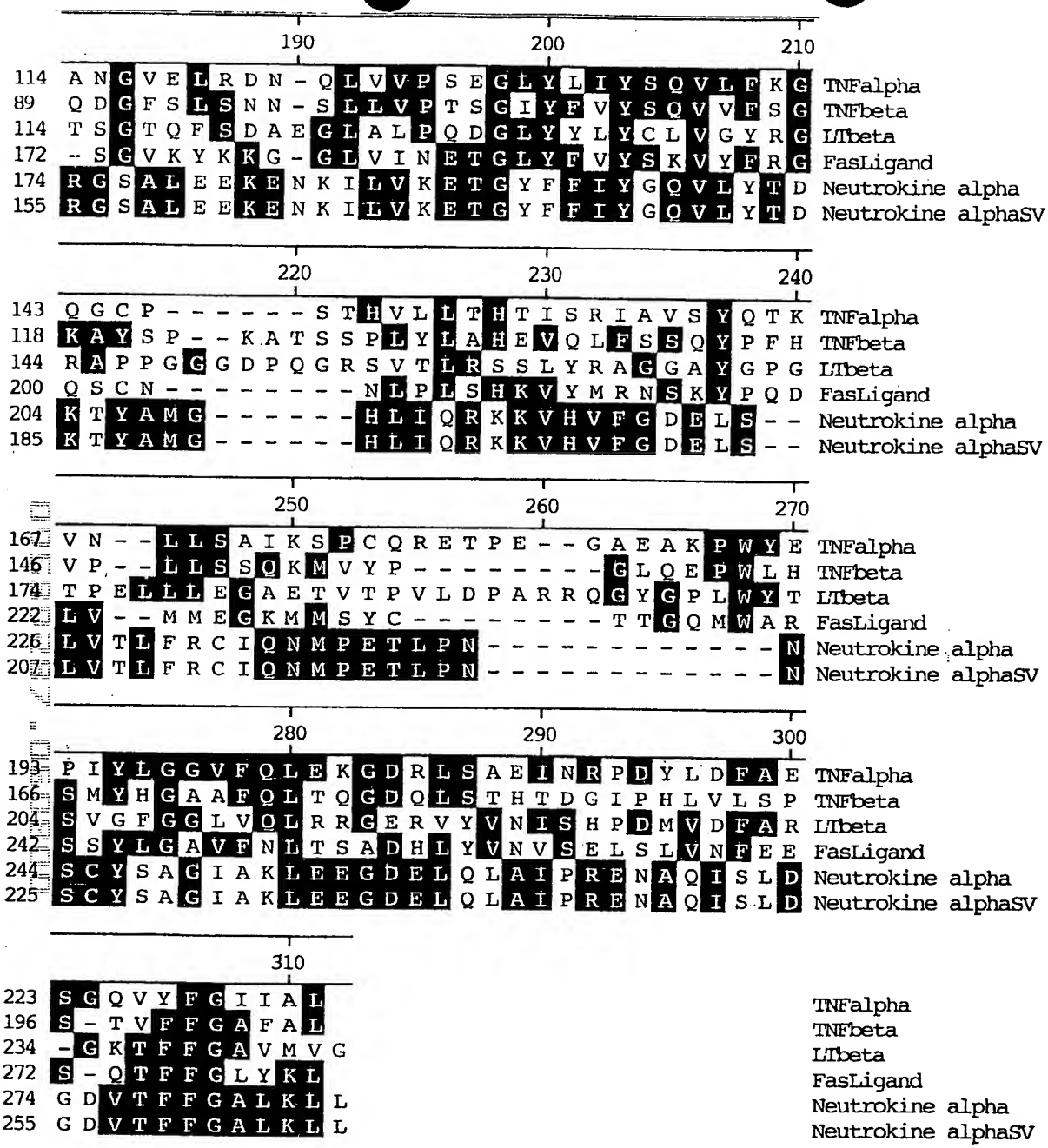

190 200 210
114 A N G V E L R D N - Q L V V P S E G L Y L I Y S Q V L F K G TNFalpha
89 Q D G F S L S N N - S L L V P T S G I Y F V Y S Q V V F S G TNFbeta
114 T S G T Q F S D A E G L A L P Q D G L Y Y L Y C L V G Y R G LTbeta
172 - S G V K Y K K G - G L V I N E T G L Y F V Y S K V Y F R G FasLigand
174 R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L Y T D Neutrokine alpha
155 R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L Y T D Neutrokine alphaSV
220 230 240
143 Q G C P - - - - - - - S T H V L L T H T I S R I A V S Y Q T K TNFalpha
118 K A Y S P - - K A T S S P L Y L A H E V Q L F S S Q Y P F H TNFbeta
144 R A P P G G G D P Q G R S V T L R S S L Y R A G G A Y G P G LTbeta
200 Q S C N - - - - - - - - - N L P L S H K V Y M R N S K Y P Q D FasLigand
204 K T Y A M G - - - - - - - H L I Q R K K V H V F G D E L S - - Neutrokine alpha
185 K T Y A M G - - - - - - - H L I Q R K K V H V F G D E L S - - Neutrokine alphaSV
250 260 270
167 V N - - L L S A I K S P C Q R E T P E - - G A E A K P W Y E TNFalpha
146 V P - - L L S S Q K M V Y P - - - - - - - - - G L Q E P W L H TNFbeta
174 T P E L L L E G A E T V T P V L D P A R R Q G Y G P L W Y T LTbeta
222 L V - - M M E G K M M S Y C - - - - - - - - - T T G Q M W A R FasLigand
226 L V T L F R C I Q N M P E T L P N - - - - - - - - - - - - - N Neutrokine alpha
207 L V T L F R C I Q N M P E T L P N - - - - - - - - - - - - - N Neutrokine alphaSV
280 290 300
193 P I Y L G G V F Q L E K G D R L S A E I N R P D Y L D F A E TNFalpha
166 S M Y H G A A F Q L T Q G D Q L S T H T D G I P H L V L S P TNFbeta
204 S V G F G G L V Q L R R G E R V Y V N I S H P D M V D F A R LTbeta
242 S S Y L G A V F N L T S A D H L Y V N V S E L S L V N F E E FasLigand
244 S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D Neutrokine alpha
225 S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D Neutrokine alphaSV
310
223 S G Q V Y F G I I A L TNFalpha
196 S - T V F F G A F A L TNFbeta
234 - G K T F F G A V M V G LTbeta
272 S - Q T F F G L Y K L FasLigand
274 G D V T F F G A L K L L Neutrokine alpha
255 G D V T F F G A L K L L Neutrokine alphaSV

Figure 3
Neutrokine-α

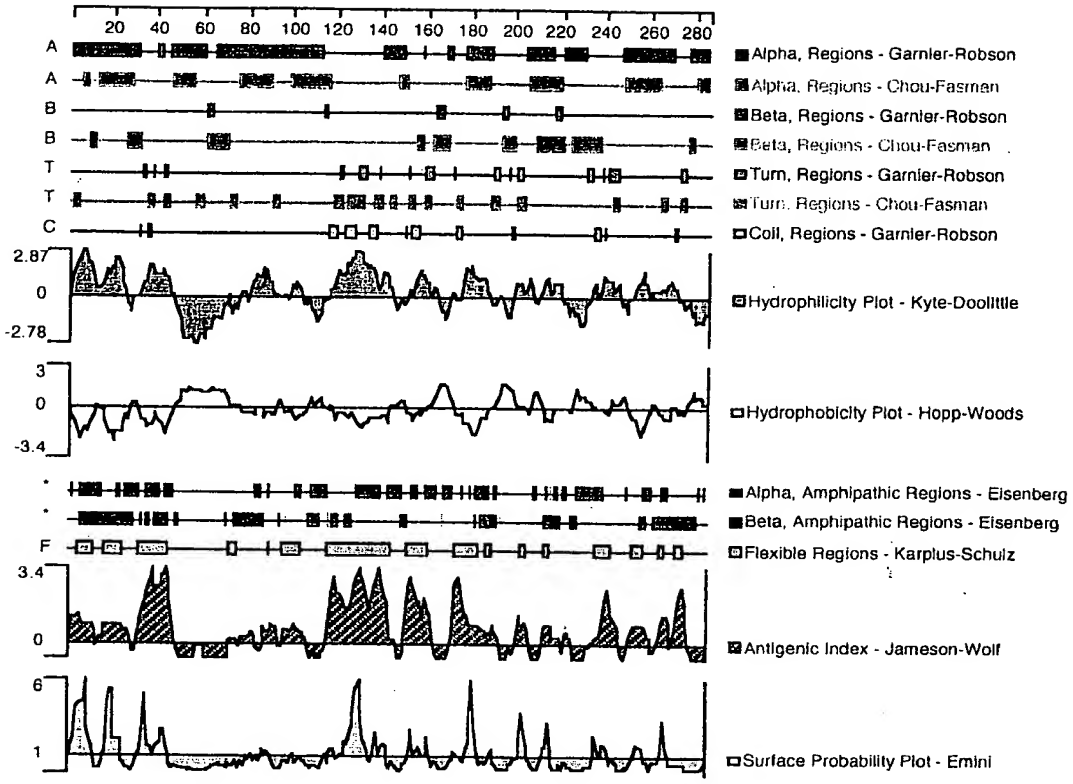


FIGURE 4 A

	1				50
HSOAD55R	.........A	GGNTAACTCT	CCTGAGGGGT	GAGCCAAGCC	CTGCCATGTA
HNEDU15X	...AAATTCA	GGATAACTCT	CCTGAGGGGT	GAGCCAAGCC	CTGCCATGTA
HSLAH84R	.AATTCGGCA	NAGNAAACTG	GTTACTTTTT	TATATATGGT	CAGGTTTTAT
HLTBM08R	AATTCGGCAC	GAGCAAGGCC	GGCCTGGAGG	AAGCTCCAGC	TGTCACCGCG

	51				100
HSOAD55R	GTGCACGCAG	GACATCANCA	A..ACACANN	NNNCAGGAAA	TAATCCATTC
HNEDU15X	GTGCACGCAG	GACATCAACA	A..ACACAGA	TAACAGGAAA	TGATCCATTC
HSLAH84R	ATACTGATAA	GACCTACGCC	ATGGGACATC	TAGTTCAGAG	GAAGAAGGTC
HLTBM08R	GGACTGAAAA	TCTTTGAACC	ACCAGCTCCA	GGAGAAGGCA	ACTCCAGTCA

	101				150
HSOAD55R	CCTGTGGTCA	CTTATTCTAA	AGGCCCCAAC	CTTCAAAGTT	CAAGTAGTGA
HNEDU15X	CCTGTGGTCA	CTTATTCTAA	AGGCCCCAAC	CTTCAAAGTT	CAAGTAGTGA
HSLAH84R	CATGTCTTTG	GGGATGAATT	GAGTCTGGTG	ACTTTGTTTC	GATGTATTCA
HLTBM08R	GAACAGCAGA	AATAAGCGTG	CCGTTCAGGG	TCCAGAAGAA	ACAGTCACTC

	151				200
HSOAD55R	TATGGATGAC	TCCACAGAAA	GGGAGCAGTC	ACGCCTTACT	TCTTGCCTTA
HNEDU15X	TATGGATGAC	TCCACAGAAA	GGGAGCAGTC	ACGCCTTACT	TCTTGCCTTA
HSLAH84R	AAATATGCCT	GAAACACTAC	CCAATAATTC	CTGCTATTCA	GCTGGCATTG
HLTBM08R	AAGACTGCTT	GCAACTGNTT	GCAGACAGTG	AAACACCAAC	TATACAAAAA

	201				250
HSOAD55R	AGAAAAGAGA	AGAAATGAAA	CTGNAAGGAG	TGTGTTTCCA	TCCTCCCACG
HNEDU15X	AGAAAAGAGA	AGAAATGAAA	CT.GAAGGAG	TGTGTTTCCA	TCCTCCCACG
HSLAH84R	CAAAACTGGN	AGGAAGGA..	...GATGAAC	TCCAACTTGC	AATACCAGGG
HLTBM08R	GGCTCCCTTC	TGNTGCCACA	TTTGGGCCAA	GGAATGGAGA	GATTTCTTCG

	251				300
HSOAD55R	GAAGGAAAGC	CCCTCTNTCC	GATCCTCCAA	AGACGGAAAG	CTGCTGGCTG
HNEDU15X	GAAGGAAAGC	CCCTCTGTCC	GATCCTCCAA	AGACGGAAAG	CTGCTGGCTG
HSLAH84R	GAAAATGCAC	AATTATCACT	GGGATGGAGA	TGTTCACATT	TTTTGGGTGC
HLTBM08R	TCTGGAAACA	TTTTGCCAAA	CTCTTCAGAT	ACTCTTTNCT	CTCTGGGAAT

	301				350
HSOAD55R	CAACCTTGNT	GNTGGCATTG	TGTTCTTGCT	GNCTCAAGGT	GGTGTTNTT.
HNEDU15X	CAACCTTGCT	GCTGGCACTG	CTGTCTTGCT	GCCTCACGGT	GGTGTCTTTC
HSLAH84R	CATTGAAACT	GCTGTGACCT	NCTTACANCA	NGTGCTGTTN	GCTATTTTNC
HLTBM08R	CAAAGGAAAA	TCTCTACTTA	GATTNACACA	TTTGTTCCCA	TGGGTNTCTT

	351				400
HSOAD55R	....	....	....	....	....
HNEDU15X	TACCAGGTGG	CCGCCCTGCA	AGGGGACCTG	GCCAGCCTCC	GGGCAGAGCT
HSLAH84R	CTNCCTNTTC	TNTGGTAACC	TCTTAGGAAG	GAAGGATTCT	TAACTGGGAA
HLTBM08R	AAGTTTTAAA	AGGGGAGTGC	CCTTAGGAGG	AAAAGGGGAT	AAATATTGGC

FIGURE 4B

```
            401                                                   450
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    GCAGGGCCAC CACGCGGAGA AGCTGCCAGC AGGAGCAGGA GCCCCCAAGG
HSLAH84R    ATAACCCAAA AAAANNTTAA ANGGGTANGN GNNANANGNG GGGNNGTTNN
HLTBM08R    CAAGGNACTG GTTANTTTNT AAATATGGTC AGGTTTNTAT ANCTGGTAGG

            451                                                   500
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    CCGGCCTGGA GGAAGCTCCA GCTGTCACCG CGGGACTGAA AATCTTTGAA
HSLAH84R    CNNGNNGNNT TTTNGGNNTA TNTTNTNNTN GGGNNNNGTA AAAATGGGGC
HLTBM08R    CCTCGCCATG GGCATTNATT CANGGNGAGG NCNNTCTTTT GGGNTGA...

            501                                                   550
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    CCACCAGCTC CAGGAGAAGG CAACTCCAGT CAGAACAGCA GAAATAAGCG
HSLAH84R    CNANGGGGGN TTTTT..... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            551                                                   600
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TGCCGTTCAG GGTCCAGAAG AAACAGTCAC TCAAGACTGC TTGCAACTGA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            601                                                   650
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TTGCAGACAG TGAAACACCA ACTATACAAA AAGGATCTTA CACATTTGTT
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            651                                                   700
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    CCATGGCTTC TCAGCTTTAA AAGGGGAAGT GCCCTAGAAG AAAAAGAGAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            701                                                   750
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TAAAATATTG GTCAAAGAAA CTGGTTACTT TTTTATATAT GGTCAGGTTT
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            751                                                   800
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TATATACTGA TAAGACCTAC GCCATGGGAC ATCTAATTCA GAGGAAGAAG
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........
```

FIGURE 4C

```
            801                                                       850
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    GTCCATGTCT TTGGGGATGA ATTGAGTCTG GTGACTTTGT TTCGATGTAT
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            851                                                       900
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TCAAAATATG CCTGAAACAC TACCCAATAA TTCCTGCTAT TCAGCTGGCA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            901                                                       950
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TTGCAAAACT GGAAGAAGGA GATGAACTCC AACTTGCAAT ACCAAGAGAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            951                                                      1000
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    AATGCACAAA TATCACTGGA TGGAGATGTC ACATTTTTTG GTGCATTGAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            1001                                                     1050
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    ACTGCTGTGA CCTACTTACA CCATGTCTGT AGCTATTTTC CTCCCTTTCT
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            1051                                                     1100
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    CTGTACCTCT AAGAAGAAAG AATCTAACTG AAAATACCAA AAAAAAAAAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            1101
HSOAD55R    ......
HNEDU15X    AAAAAA
HSLAH84R    ......
HLTBM08R    ......
```

Figure 5A
Neutrokine-αSV

```
   1  ATGGATGACTCCACAGAAAGGGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAA   60
   1  M  D  D  S  T  E  R  E  Q  S  R  L  T  S  C  L  K  K  R  E    20

  61  GAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCCACGGAAGGAAAGCCCCTCTGTCCGA  120
  21  E  M  K  L  K  E  C  V  S  I  L  P  R  K  E  S  P  S  V  R    40
                                    CD-I

 121  TCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGC  180
  41  S  S  K  D  G  K  L  L  A  A  T  L  L  L  A  L  L  S  C  C    60
         CD-I

 181  CTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGG  240
  61  L  T  V  V  S  F  Y  Q  V  A  A  L  Q  G  D  L  A  S  L  R    80
                                          CD-II

 241  GCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCCAAGGCC  300
  81  A  E  L  Q  G  H  H  A  E  K  L  P  A  G  A  G  A  P  K  A   100
         CD-II                                   CD-III

 301  GGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACTGAAAATCTTTGAACCACCAGCTCCA  360
 101  G  L  E  E  A  P  A  V  T  A  G  L  K  I  F  E  P  P  A  P   120
      CD-III
               #
 361  GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTCAGGGTCCAGAAGAA  420
 121  G  E  G  N  S  S  Q  N  S  R  N  K  R  A  V  Q  G  P  E  E   140

 421  ACAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAA  480
 141  T  G  S  Y  T  F  V  P  W  L  L  S  F  K  R  G  S  A  L  E   160
                                    CD-IV

 481  GAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTTTTTTATATATGGTCAGGTT  540
 161  E  K  E  N  K  I  L  V  K  E  T  G  Y  F  F  I  Y  G  Q  V   180
      CD-IV                          CD-V

 541  TTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGTCCATGTC  600
 181  L  Y  T  D  K  T  Y  A  M  G  H  L  I  Q  R  K  K  V  H  V   200
                  CD-VI                  CD-VII

 601  TTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAAATATGCCTGAAACA  660
 201  F  G  D  E  L  S  L  V  T  L  F  R  C  I  Q  N  M  P  E  T   220
      CD-VIII                        CD-VIII
            #
 661  CTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAAAACTGGAAGAAGGAGATGAACTC  720
 221  L  P  N  N  S  C  Y  S  A  G  I  A  K  L  E  E  G  D  E  L   240
                     CD-IX                  CD-X

 721  CAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTT  780
 241  Q  L  A  I  P  R  E  N  A  Q  I  S  L  D  G  D  V  T  F  F   260
               CD-X                                    CD-XI

 781  GGTGCATTGAAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCCTCCCTTTC  840
 261  G  A  L  K  L  L                                              266
            CD-XI
```

Figure 5B
Neutrokine-αSV

841 TCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAAAAA 900

901 AAA 903

Figure 6
Neutrokine-αSV

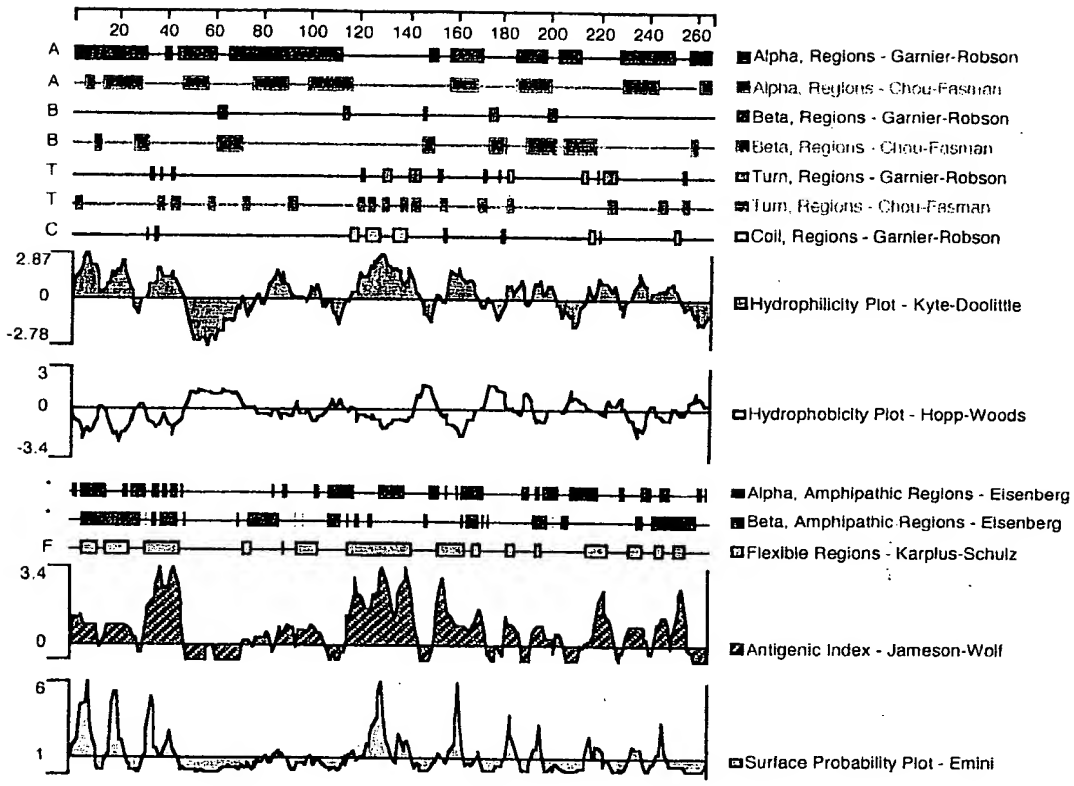
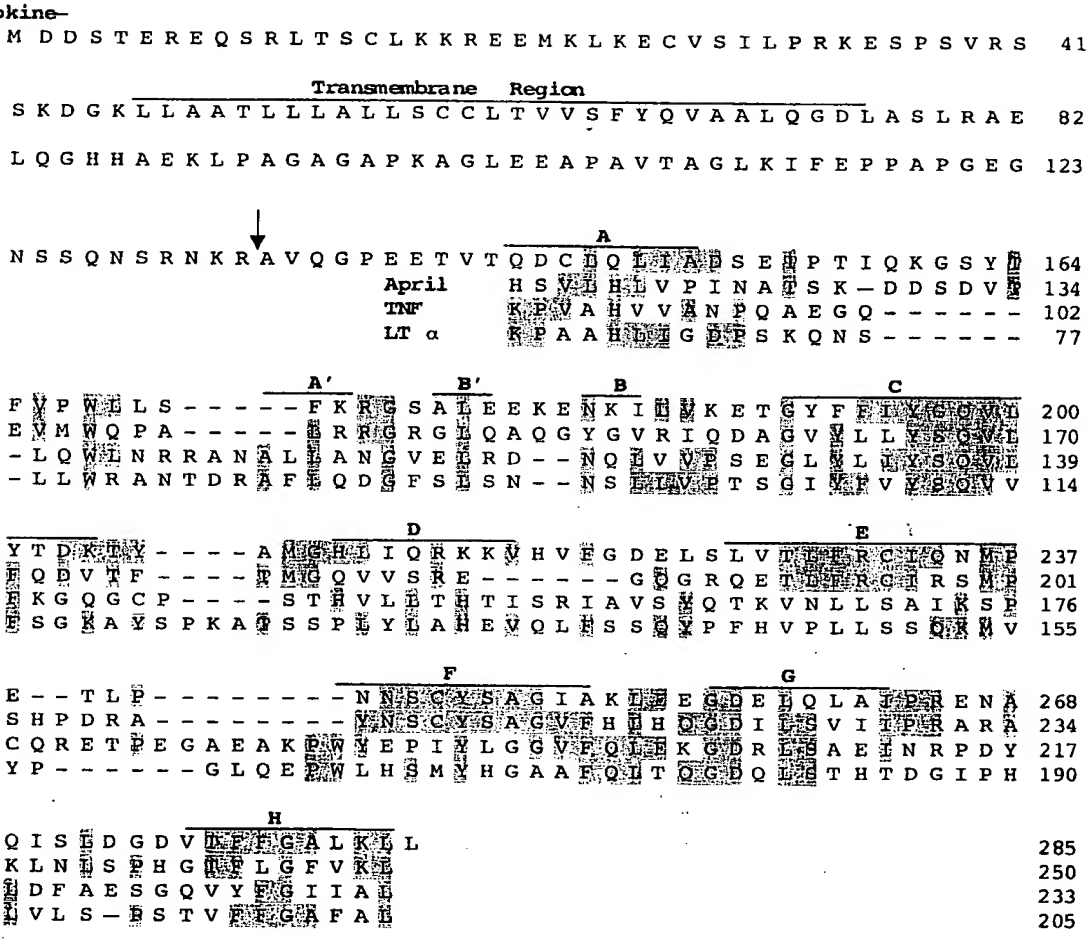


Figure 7

a.


leutrokine-
ılpha M D D S T E R E Q S R L T S C L K K R E E M K L K E C V S I L P R K E S P S V R S 41
Transmembrane Region
S K D G K L L A A T L L L A L L S C C L T V V S F Y Q V A A L Q G D L A S L R A E 82
L Q G H H A E K L P A G A G A P K A G L E E A P A V T A G L K I F E P P A P G E G 123
A
N S S Q N S R N K R A V Q G P E E T V T Q D C L Q L I A D S E T P T I Q K G S Y T 164
April H S V L H L V P I N A T S K - D D S D V T 134
TNF K P V A H V V A N P Q A E G Q - - - - - - - 102
LT α K P A A H L I G D P S K Q N S - - - - - - - 77
A' B' B C
F Y P W L L S - - - - - F K R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L 200
E V M W Q P A - - - - - E R R G R G L Q A Q G Y G V R I Q D A G V Y L L Y S Q V L 170
- L Q W L N R R A N A L L A N G V E L R D - - N Q L V V P S E G L Y L I Y S Q V L 139
- L L W R A N T D R A F L Q D G F S L S N - - N S L L V P T S G I Y F V Y S Q V V 114
D E
Y T D K T Y - - - - A M G H L I Q R K K V H V F G D E L S L V T L F R C I Q N M P 237
E Q D V T F - - - - P M G Q V V S R E - - - - - - - G Q G R Q E T L F R C I R S M P 201
E K G Q G C P - - - - S T H V L L T H T I S R I A V S Y Q T K V N L L S A I K S P 176
E S G K A Y S P K A G S S P L Y L A H E V Q L H S S Q Y P F H V P L L S S Q K M V 155
F G
E - - T L P - - - - - - - - - N N E C Y S A G I A K L E E G D E L Q L A I P R E N A 268
S H P D R A - - - - - - - - - V N S C Y S A G V F H L E K G D I L S V I I P R A R A 234
C Q R E T P E G A E A K P W Y E P I Y L G G V F Q L E K G D R L S A E I N R P D Y 217
Y P - - - - - - G L Q E P W L H S M Y H G A A F Q L T Q G D Q L S T H T D G I P H 190
H
Q I S L D G D V L F T C A L K L L 285
K L N L S P H G L F L G F V K L 250
L D F A E S G Q V Y F G I I A L 233
L V L S - P S T V F F G A F A L 205

b.

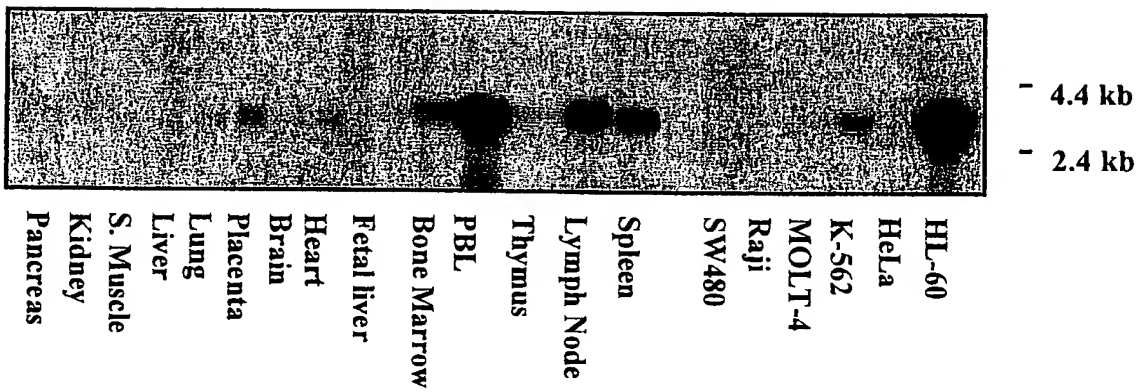
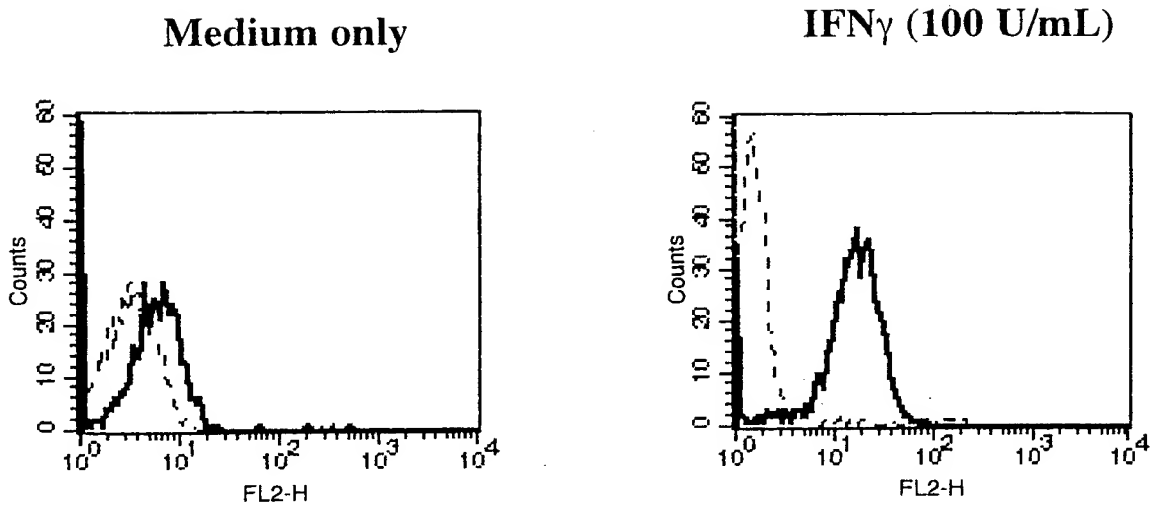

4.4 kb
2.4 kb
Pancreas
Kidney
S. Muscle
Liver
Lung
Placenta
Brain
Heart
Fetal liver
Bone Marrow
PBL
Thymus
Lymph Node
Spleen
SW480
Raji
MOLT-4
K-562
HeLa
HL-60

Figure 8

a.


Medium only
IFNγ (100 U/mL)
Counts
FL2-H

b.

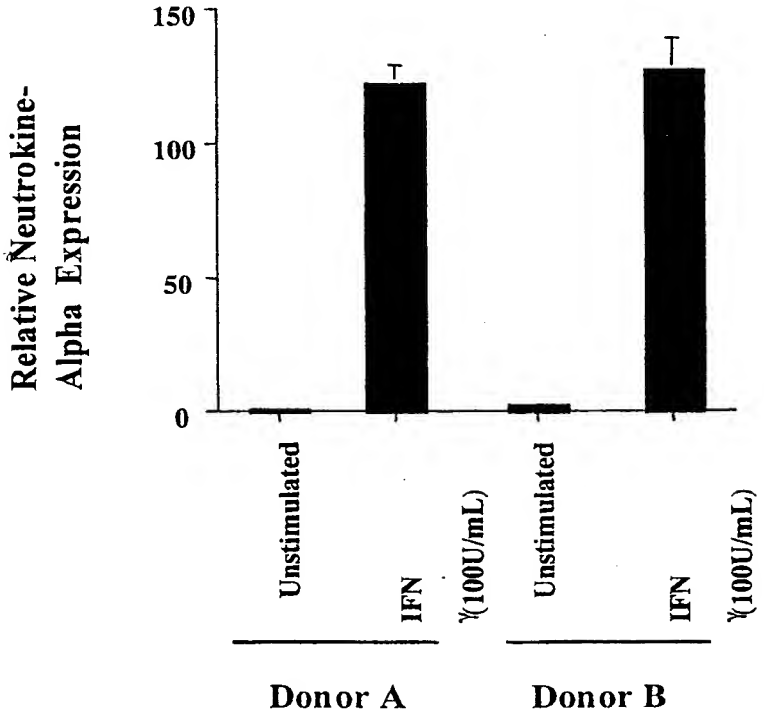
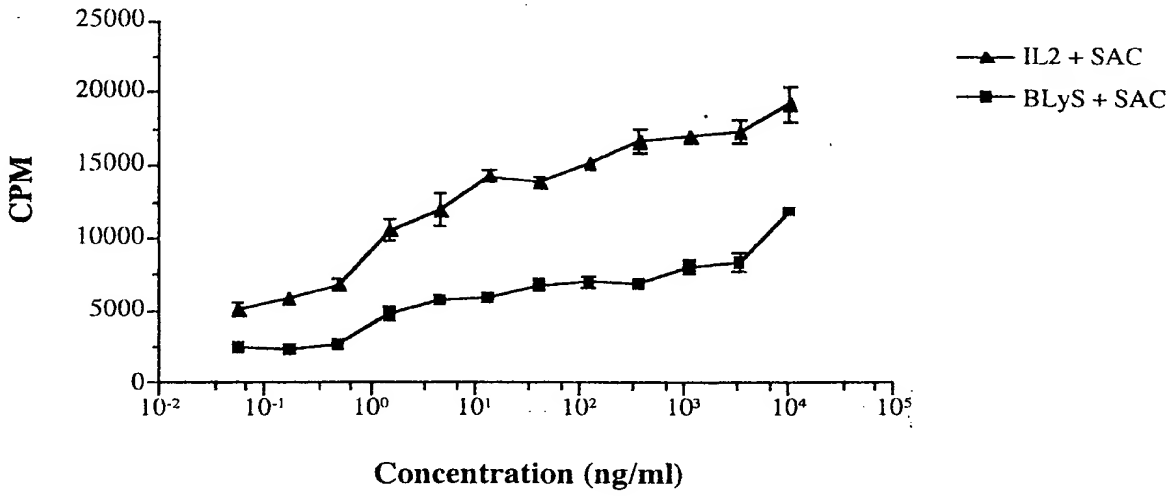

Relative Neutrokine-Alpha Expression
150
100
50
0
Unstimulated
IFN γ(100U/mL)
Donor A
Donor B

Figure 9

a.


25000
20000
15000
10000
5000
0
CPM
10^{-2}
10^{-1}
10^{0}
10^{1}
10^{2}
10^{3}
10^{4}
10^{5}
Concentration (ng/ml)
IL2 + SAC
BLyS + SAC

b.

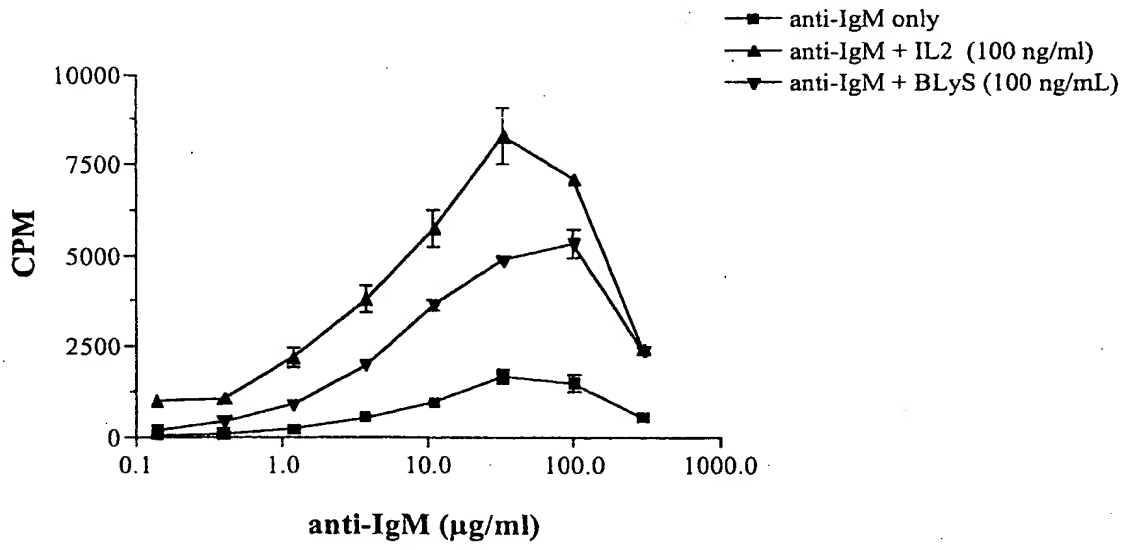
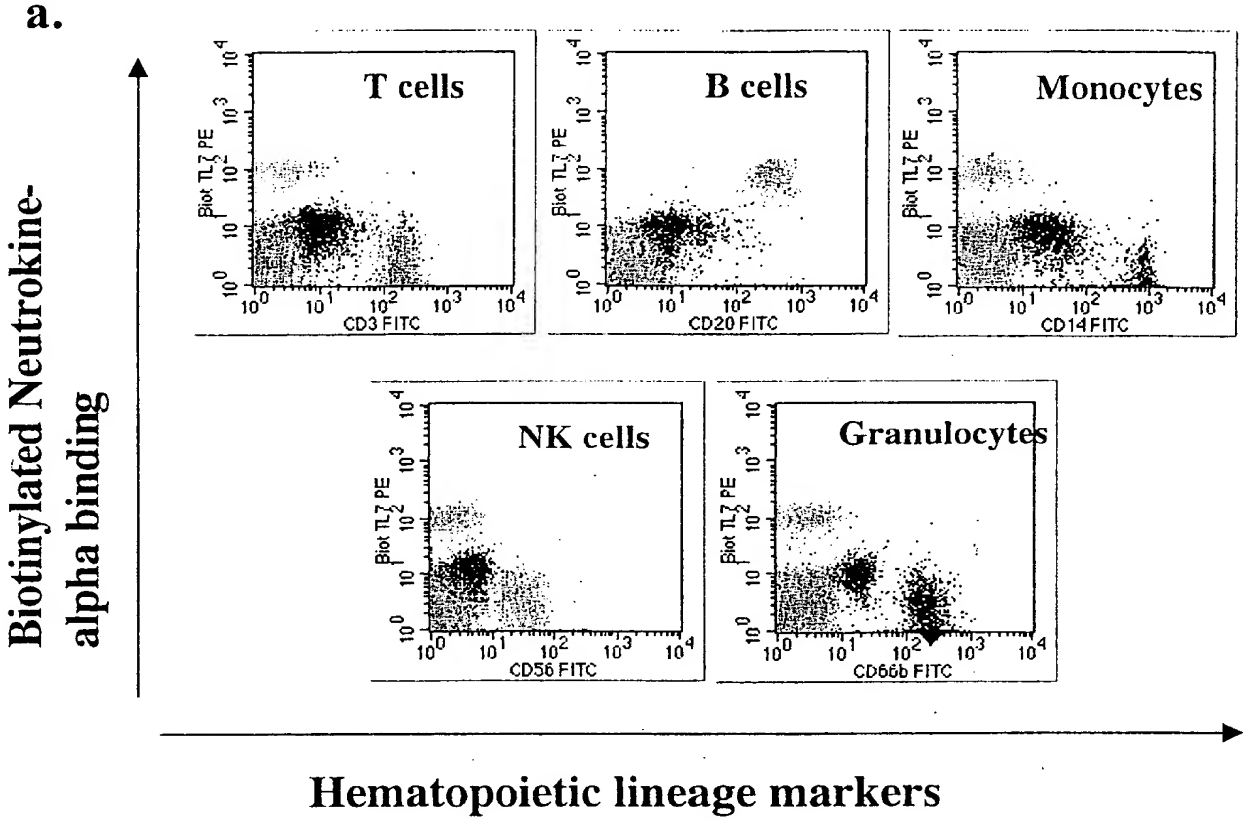

10000
7500
5000
2500
0
CPM
0.1
1.0
10.0
100.0
1000.0
anti-IgM (µg/ml)
anti-IgM only
anti-IgM + IL2 (100 ng/ml)
anti-IgM + BLyS (100 ng/mL)

Figure 10

a.


T cells
B cells
Monocytes
NK cells
Granulocytes
Biot TL2 PE
CD3 FITC
CD20 FITC
CD14 FITC
CD56 FITC
CD66b FITC
Biotinylated Neutrokine-alpha binding
Hematopoietic lineage markers

b.

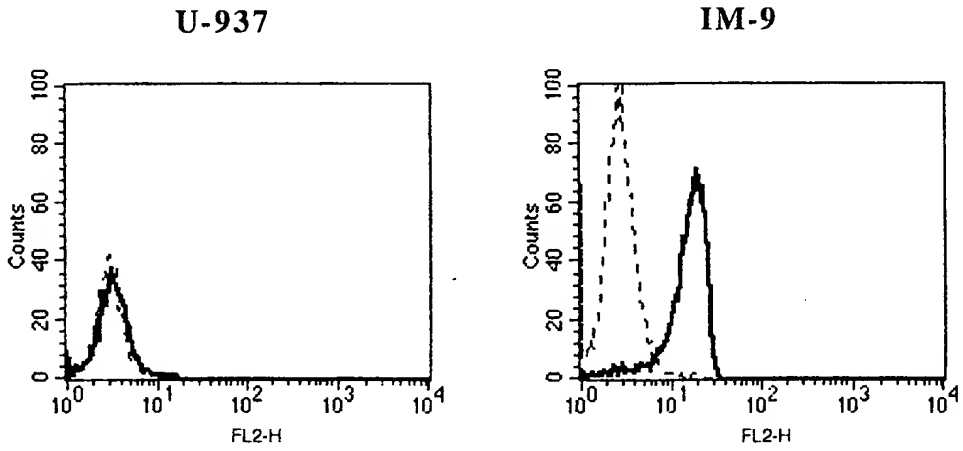
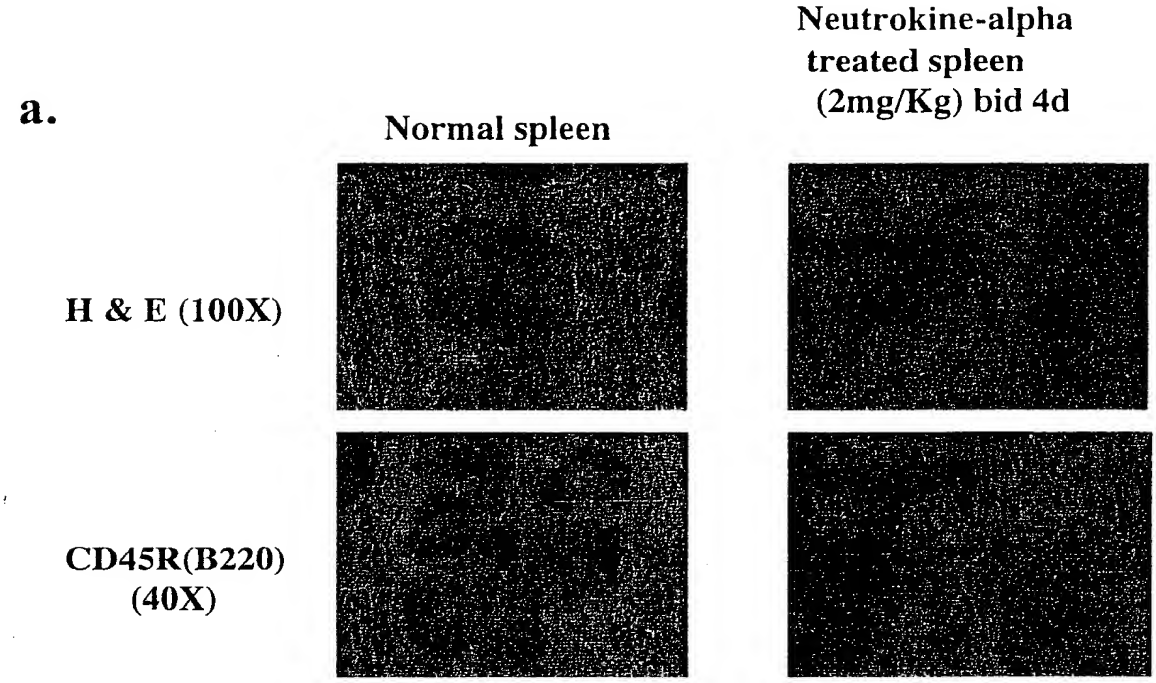

U-937
IM-9
Counts
FL2-H

Figure 11


a.
Normal spleen
Neutrokine-alpha treated spleen (2mg/Kg) bid 4d
H & E (100X)
CD45R(B220) (40X)
b.
Normal BALB/c
Neutrokine-alpha treated BALB/c
CD45R (B220)
ThB (Ly6D)
c.
IgM
IgA
IgG
Serum IgM (ug/mL)
Serum IgA (ug/mL)
Serum IgG (ug/mL)
Buffer
Neutrokine-alpha